File 155:MEDLINE(R) 1951-2006/Feb 21
(c) format only 2006 Dialog
***File 155: Medline has resumed updating.**
File 55:Biosis Previews(R) 1993-2006/Feb W2
(c) 2006 BIOSIS
File 34:SciSearch(R) Cited Ref Sci 1990-2006/Feb W2
(c) 2006 Inst for Sci Info
File 434:SciSearch(R) Cited Ref Sci 1974-1989/Dec
(c) 1998 Inst for Sci Info
File 340:CLAIMS(R)/US Patent 1950-06/Feb 16
(c) 2006 IFI/CLAIMS(R)
***File 340: IPCR/8 classification codes now** searchable in 2006 records.
For important information about IC=index changes, see HELP NEWSIPCR.

Set	Items	Description
? s genome(w)cryptographer		
	338748	GENOME
	11	CRYPTOGRAPHER
S1	5	GENOME(W)CRYPTOGRAPHER

? rd

>>>Duplicate detection is not supported for File 340.

>>>Records from unsupported files will be retained in the RD set.
S2 3 RD (unique items)
? t s2/3,k,ab/1-3

2/3,K,AB/1 (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
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15015738 PMID: 14559213
Genome sequence and splice site analysis of low-fidelity DNA polymerases H and I involved in replication of damaged DNA.
Cleaver J E; Collins C; Ellis J; Volik S
UCSF Cancer Center, Box 0808, Room N431, University of California at San Francisco, San Francisco, CA 94143-0808, USA. jcleaver@cc.ucsf.edu
Genomics (United States) Nov 2003, 82 (5) p561-70, ISSN 0888-7543 Journal Code: 8800135
Contract/Grant No.: 1 R01 ES 8061; ES; NIEHS
Publishing Model Print
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: MEDLINE; Completed
POLH and POLI are paralogs encoding low-fidelity, class Y, DNA polymerases involved in replication of damaged DNA in the human disease xeroderma pigmentosum variant. Analysis of genomic regions for human and mouse homologs, employing the analytic tool **Genome Cryptographe**r , detected low-repetitive or unique regions at exons and other potential control regions, especially within intron I of human POLH. The human and mouse homologs are structurally similar, but the paralogs have undergone evolutionary divergence. The information content of splice sites for human POLH, the probability that a base would contribute to splicing, was low only for the acceptor site of exon II, which is preceded by a region of high information content that could contain sequences controlling splicing. This analysis explains previous observations of tissue-specific skipping during mRNA processing, resulting in the loss of the transcription start

site in exon II, in human tissues.

... pigmentosum variant. Analysis of genomic regions for human and mouse homologs, employing the analytic tool **Genome Cryptographer** , detected low-repetitive or unique regions at exons and other potential control regions, especially within...

2/3,K,AB/2 (Item 1 from file: 55)
DIALOG(R)File 55:Biosis Previews(R)

0013825970 BIOSIS NO.: 200200419481
Genomic analysis of prostate tumors using whole genome and 16q contig array CGH and genome cryptographer
AUTHOR: Watson Vivienne (Reprint); Kowbel David; Paris Pamela; Andaya Armann; Volik Stanislav; Kamkar Sherwin; James Karen; Sudilovsky Daniel; Schmitt Lars; Shuman Marc; Carroll Peter; Doggett Norman; Rosenburg Carla ; van Dekken Herman; Gray Joe; Albertson Donna; Pinkel Daniel; Collins Colin
AUTHOR ADDRESS: UCSF Cancer Center, San Francisco, CA, USA**USA
JOURNAL: Proceedings of the American Association for Cancer Research Annual Meeting 43 p1067 March, 2002 2002
MEDIUM: print
CONFERENCE/MEETING: 93rd Annual Meeting of the American Association for Cancer Research San Francisco, California, USA April 06-10, 2002; 20020406
ISSN: 0197-016X
DOCUMENT TYPE: Meeting; Meeting Abstract
RECORD TYPE: Citation
LANGUAGE: English

Genomic analysis of prostate tumors using whole genome and 16q contig array CGH and genome cryptographer
DESCRIPTORS:
...METHODS & EQUIPMENT: **genome cryptographer** --

2/3,K,AB/3 (Item 2 from file: 55)
DIALOG(R)File 55:Biosis Previews(R)

0013565517 BIOSIS NO.: 200200159028
1Mb spanning a 20q13.2 breast cancer amplicon: Novel sequence analysis tools
AUTHOR: Collins Colin (Reprint); Volik Stanislav; Kowbel David; Kuo Wen-Lin ; Gray Joe
AUTHOR ADDRESS: UCSF Cancer Center, San Francisco, CA, USA**USA
JOURNAL: Cytometry Supplement (10): p181-182 2000 2000
MEDIUM: print
CONFERENCE/MEETING: The XX Congress of the International Society for Analytical Cytology Montpellier, France May 20-25, 2000; 20000520
SPONSOR: International Society for Analytical Cytology
ISSN: 1046-7386
DOCUMENT TYPE: Meeting; Meeting Abstract
RECORD TYPE: Citation
LANGUAGE: English

DESCRIPTORS:

...METHODS & EQUIPMENT: **Genome** **Cryptographer** --
?

12/3,K,AB/4 (Item 4 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07261940 PMID: 4001930
The mosaic genome of warm-blooded vertebrates.
Bernardi G; Olofsson B; Filipski J; Zerial M; Salinas J; Cuny G; Meunier-Rotival M; Rodier F
Science (UNITED STATES) May 24 1985, 228 (4702) p953-8, ISSN 0036-8075 Journal Code: 0404511
Publishing Model Print
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: MEDLINE; Completed
Most of the nuclear genome of warm-blooded vertebrates is a mosaic of very long (much greater than 200 kilobases) DNA segments, the isochores; these isochores are fairly homogeneous in base composition and belong to a small number of major classes distinguished by differences in guanine-cytosine (GC) content. The families of DNA molecules derived from such classes can be separated and used to study the genome distribution of any sequence which can be probed. This approach has revealed (i) that the distribution of genes, integrated viral sequences, and interspersed repeats is highly nonuniform in the genome, and (ii) that the base composition and ratio of **CpG** to GpC in both coding and noncoding sequences, as well as codon usage, mainly depend on the GC content of the isochores harboring the sequences. The compositional compartmentalization of the genome of warm-blooded vertebrates is discussed with respect to its evolutionary origin, its causes, and its effects on chromosome structure and function.

...is highly nonuniform in the genome, and (ii) that the base composition and ratio of **CpG** to GpC in both coding and noncoding sequences, as well as codon usage, mainly depend...

; Animals; Base Composition; Base Sequence; Centrifugation, **Density** Gradient; Chromosome Banding; Codon; Cytosine--analysis--AN; DNA--analysis --AN; DNA Replication; DNA, Viral--genetics--GE; Evolution; **Gene Amplification** ; Genes, Viral; Guanine--analysis--AN; Humans; Mice --genetics--GE; Mutation; Rabbits--genetics--GE; Recombination, Genetic...
?